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July 26, 2000

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Dear Sir:

Enclosed please find the following documents relating to the application of Li Xing and Robert C. Glen entitled *Method For Accurately Estimating pK_a Of Molecules Using Atom Type Definitions And Partial Least Squares*:

1. a patent specification of 15 pages including the cover page, one table, and the Abstract and claiming the benefit of an earlier filed U.S. Provisional application;
2. an Appendix of 8 pages containing SPL software script;
3. 9 figures on 9 sheets;
4. a return post card; and
5. an Express Mail certificate.

Please address all correspondence regarding this patent application to me at the address set out above.

Respectfully submitted,

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION

OF

LI XING

AND

ROBERT C. GLEN

FOR

METHOD FOR ACCURATELY ESTIMATING pK_a OF MOLECULES

USING ATOM TYPE DEFINITIONS AND PARTIAL LEAST SQUARES

METHOD FOR ACCURATELY ESTIMATING pK_a OF MOLECULES USING ATOM TYPE DEFINITIONS AND PARTIAL LEAST SQUARES

Benefit of U.S. Provisional Application No. 60/145,595 filed July 26, 1999 is hereby
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rights whatsoever.

FIELD OF THE INVENTION

This invention relates to the calculation from the molecular structure of the pK_a of
molecules which contain an ionizable group. More specifically, the pK_a is estimated by
applying the coefficients derived by the PLS (Partial Least Squares) statistical methodology
from a training set of compounds with known pK_a s to the hierarchical connectivity
15 characteristic of the molecule of interest.

BACKGROUND OF THE INVENTION

The bio-availability of a drug to the therapeutic target is an important consideration in
rational drug design. Before a drug elicits an effect, it has to pass through various cellular
barriers either by passive diffusion and/or by carrier-mediated uptake. Depending on the
20 location of the target site, the pH of the environment may vary considerably. Many
molecules of biological interest contain acidic and/or basic groups which govern their
biological properties. In particular, the ability of molecules to cross biological membranes is

governed in part by the ionization state of the molecule in the pH of the surrounding medium. The proportion of neutral and charged molecular species present at a given pH is determined by the pK_a value. The pK_a can be determined by laborious and detailed measurements or by an empirical system of estimation developed over the years by Perrin et. al. With the advent of combinatorial synthesis and high throughput screening, the number of molecules for which it is desirable to know the pK_a far exceeds the ability to synthesize the molecules and experimentally determine the pK_a .

SUMMARY OF THE INVENTION

What has been needed for some time is a simple, fast, and reliable method to estimate pK_a with a high degree of accuracy for any molecule including molecules with more than one ionizable moiety. The present invention accomplishes the estimation of pK_a with such accuracy and speed. Using the idea that the degree of ionization of a particular group depends upon its sub-environment (which is comprised of the neighboring atoms and bonds), a hierarchical tree may be constructed from the ionizing atom outwards. This tree contains atoms directly connected to the root atoms at the first level, those bonded to the first level at the second level, and so on. The estimation of pK_a is accomplished by constructing for each molecule in a training set the hierarchical tree and applying the Partial Least Squares statistical methodology as implemented in the SYBYL software program to this group of molecules for which a measured pK_a is available to extract predictive coefficients.

DESCRIPTION OF FIGURES

Figure 1 schematically outlines the procedure for determining a hierarchical connectivity definition for a molecule starting from an ionizable center.

Figure 2 is a list of typical atom and group type definitions used to construct the hierarchical connectivity definition for a molecule.

Figure 3 shows a molecular representation of the group type definitions of Figure 2.

Figure 4 shows how the hierarchical connectivity definition for 6-amino quinoline is placed within a table of levels of atom connectivity and group type definitions.

Figure 5 shows how the hierarchical connectivity definition for an imidazole is placed within a table of levels of atom connectivity and group type definitions.

Figure 6 shows how the hierarchical connectivity tree is defined for 6-amino quinoline.

Figure 7 shows a scatter plot of predicted versus measured values for the pK_a of bases.

Figure 8 shows a scatter plot of predicted versus measured values for the pK_a of acids.

Figure 9 shows a scatter plot of the predicted versus measured values of 37 compounds which were not included in the training set for the method of the present invention. Two sets of predicted values are shown, those derived by the method of the present invention and those derived by the method of Perrin.

DETAILED DESCRIPTION OF THE INVENTION

For each molecule in the training set group, a hierarchical tree of atom connectivities found in the molecule is constructed, starting from an ionizable center, which reflects the atom types at each level of connectivity. The overall procedure is schematically indicated in Figure 1. Since each of the molecular hierarchical connectivity definitions is associated with

a measured pK_a , the system is complex and a statistical methodology must be used to extract a predictive model. Depending on the size of the training sample, the system may be over determined or under determined. The result of applying PLS to a group (training set) of molecules is the determination of coefficients associated with each atom type at each of the hierarchical levels which reflects the contribution of that atom type at that level to the final pK_a . To predict the pK_a for a molecule not included in the original group, the atom type connectivity for that molecule is determined and for each bin the number of occurrences of the atom type in the bin is multiplied by the corresponding PLS determined coefficient for that bin. The sum of the individual bin multiplications over all the bins is the predicted pK_a .

Many different atom type definitions may be used, but the inventors have found the types set out in Figure 2 to be most useful. 25 atom types are defined along with 7 group types. The group types are also shown in Figure 3. Most molecules of biological interest can be defined with these 32 types. Examples for defining the atom type connections for two molecules are shown in Figure 4 and Figure 5. At each level, the number of times each atom type occurs at that level is noted in the appropriate "bin." Thus, for 6-amino quinoline, shown in Figure 4 and Figure 6, the ionizable nitrogen of interest is defined as an aromatic nitrogen at level 0. Level 1 includes the two aromatic carbons attached to the level 0 nitrogen. Level 3 finds one hydrogen attached to an aromatic carbon, and three different aromatic carbons. This process of definition may be continued for as many additional hierarchical levels as desired. The inventors have found that 5 levels beyond the initial zero level produce very good results. Using the atom type definitions found in Figure 2, 32 possible atom type bins are available at each level. However, for level 0, only 20 bins are

necessary since the tree would never start with hydrogen, halogens, or group types. The maximum number of bins which could be used for the atom type definitions set out in Figure 2 would be $[(5 \times 32) + 20] = 180$. Clearly, for other atom type definitions, a greater or lesser number of bins could be used to form the molecular "fingerprint". Also, if a particular atom type does not occur in the training sample, that atom type will be excluded from further use. One of the interesting properties of the method of this invention is that it can still predict with reasonable accuracy the pK_a of a molecule which has an atom type within it which was not found in the training sample. Typically, only approximately 50% of the atom types may be found in a training sample.

Once the fingerprints for all molecules in the initial training group have been determined, the fingerprints along with the measured pK_a for each molecule are analyzed with PLS using a cross-validation procedure. Generally, when using PLS, a sufficient number of components are extracted to yield a cross-validated q^2 of at least 0.5. As can be seen in Figure 7, when 384 bases were used in the training sample, 5 principal components yielded a q^2 of 0.832. As shown in Figure 8, a sample of 646 acids using 6 principal components yielded a q^2 of 0.792. These results are statistically significant. Further, the scatter plots shown in Figure 7 and Figure 8 clearly demonstrate that the method is highly predictive. The solid line represents the ideal correlation between predicted and measured values. The predictive values shown are the result of the PLS analysis.

As noted, the result of using PLS with the training sample is the generation of a coefficient for each of the bins which reflects the contribution of the atom type in that bin to the total pK_a . For the imidazole shown in Figure 5, multiplying the number of occurrences of

each atom type in the hierarchical definition by the coefficient determined by PLS for each bin and summing the result, yields a predicted pK_a of 6.63. This corresponds well to the measured pK_a of 6.04. Predicted versus measured pK_a s using the method of Perrin and the method of this invention are set out in Table 1 and as a scatter plot in Figure 9.

5 The coefficients found from the training sample by PLS will, of course, vary somewhat with the molecules in the training sample. However, for a sufficiently large and diverse training sample, such variation will be minimal. The method of this invention thus allows the simple, rapid, and highly accurate determination of the pK_a for any molecule of interest.

10 All computations including the hierarchical connectivity definitions, the PLS analysis, and the PLS prediction are implemented in a modern computational chemistry environment using software designed to handle molecular structures and associated properties and operations. For purposes of this Application, such an environment is specifically referenced. In particular, the computational environment and capabilities of the *SYBYL* software program developed and marketed by Tripos, Inc. (St. Louis, Missouri) is specifically utilized. The software script written in SPL (*SYBYL* Programming Language) to implement the functionality of the disclosed method is provided in an Appendix to this Application. Software with similar functionalities to *SYBYL* is available from other sources, both commercial and non-commercial, well known to those in the art. In addition to *SYBYL*,
15 other commercial software packages are available to implement PLS. A general purpose programmable digital computer with ample amounts of memory and hard disk storage is required for the implementation of this invention.
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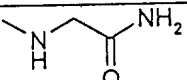
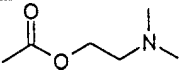
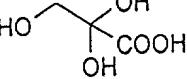
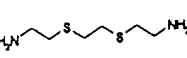
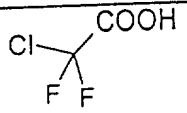
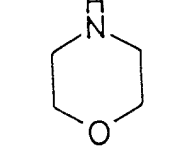
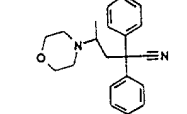
TABLE 1

Prediction of pKa values of substituted aliphatic acids and bases:

Acid strengthening: $-\Delta \text{pKa} = 0.06 + 0.63 \sigma^*$ Base-weakening: $-\Delta \text{pKa} = 0.28 + 0.87 \sigma^*$

Name	Structure	Perrin	Model	Measured	Comment
Bis(2-chloroethyl)(2-methoxyethyl)amine		5.10	6.54	5.45	
1-(4'-hydroxycyclohexyl)-2-(isopropylamino)ethanol		9.99	11.49	10.23	PKa for amino
2-aminocycloheptanol		9.67	10.75	9.25	PKa for amino
N,N-dimethyl-2-butyne-1-amine		~ 8.1	10.44	8.28	
5-amino-3-azapentanol		9.87	9.85	9.82	PKa1: 5-amino; pKa2: 3-azo Predicted pKa2: 9.29
5-chloro-3-methyl-3-azapentanol		7.1	8.53	7.48	PKa for amino
Hexamethylenetetramine		~ 6.0	11.35	6.2	
2-acetylbutanedioic acid		3.15	3.19	2.86	PKa1: 1- COOH; pKa2: 4- COOH Predicted pKa2: 3.68
Methionine		2.20 9.33	2.20 9.29	2.17 9.20	PKa1: COOH PKa2: amino
Piperazine		9.85	9.61	9.78	

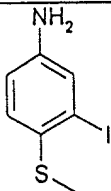
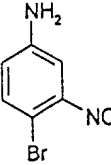
The Taft equation: $pK = pK^0 - \rho^* \Sigma(\sigma^*)$

Name	Structure	Perrin	Model	Measured	Comment
2-(methylamino)acetamide		8.43	9.07	8.31	PKa for amino
2-(dimethylamino)ethyl acetate		8.26	8.38	8.35	PKa for amino
2,3-dihydroxy-2-hydroxymethylpropanoic acid		3.01	3.42	3.29	Pka for COOH
1,8-diamino-3,6-dithiaoctane		9.06	9.62	9.47	
Chlorodifluoroacetic acid		0.82	1.47	0.46	
Morpholine		8.92	8.92	8.36	
4-morpholino-2,2-diphenylpentanenitrile		6.38	6.51	6.05	

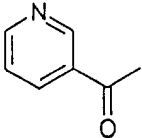
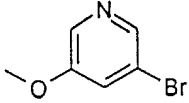
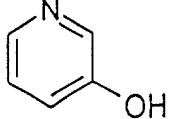
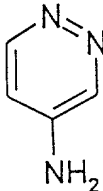
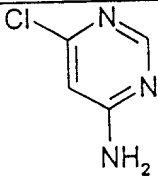
Prediction of pKa values for phenols, aromatic carboxylic acids and aromatic amines

The Hammett equation: $pK_a = pK_a^0 - \rho(\Sigma\sigma)$

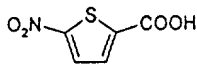
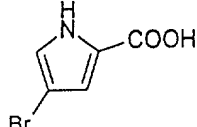
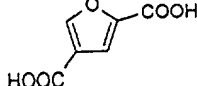
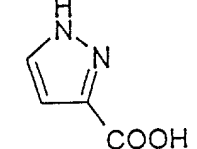
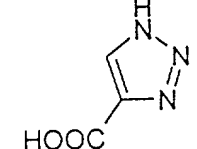
Name	Structure	Perrin	Model	Measured	Comment
4-chloro-3,5-dimethylphenol		9.70	9.11	9.71	
Pyrogallol		9.24	9.02	9.12	PKa1: 1- or 3- OH; PKa2: 2- OH Predicted pKa2: 9.54
Benzenhexol		8.31	8.60	9.0	
Picric acid		0.91	2.89	0.33	
2,6-dichloro-1,4-benzenediol		6.82	6.50	7.30	PKa1: 1- OH; pKa2: 4- OH Predicted pKa2: 7.85
3,4,5-trihydroxybenzoic acid		4.32	3.46	4.46	PKa1: COOH; pKa2: 3- or 5- OH; pKa3: 4- OH Predicted pKa2: 8.80, pKa3: 9.47
4-bromo-1,2-benzenedicarboxylic acid		2.86	2.74	2.5	PKa1: 2- COOH; pKa2: 1- COOH Predicted pKa2: 3.48
4-hydroxy-3,5-dimethoxybenzoic acid		4.36	4.30	4.34	PKa1: COOH; pKa2: 4- OH Predicted pKa2: 7.13

3-iodo-4-methylthioaniline		3.34	3.44	3.44	
4-bromo-3-nitroaniline		1.82	1.80	1.80	

Prediction of pKa values of heteroaromatic acids and bases by the Hammett and Taft equations.

Name	Structure	Perrin	Model	Measured	Comment
3-acetylpyridine		3.13	4.43	3.26	
3-bromo-5-methoxypyridine		2.30	2.50	2.60	
3-hydroxypyridine		4.48 8.29	4.86 11.78	4.80 8.74	
4-aminopyridazine		5.31	6.66	6.65	PKa1: 1- N; pKa2: 2- N Predicted pKa2: 3.64
4-amino-6-chloropyrimidine		1.41	3.52	2.10	PKa1: 3- N; pKa2: 1- N Predicted pKa2: 1.30

Extension of the Hammett and Taft equations to heterocycles.

Name	Structure	Perrin	Model	Measured	Comment
4-nitrothiophen-2-carboxylic acid		2.70	2.44	2.68	
4-bromopyrrol-2-carboxylic acid		4.05	3.62	4.06	PKa for COOH
Furan-2,4-dicarboxylic acid		2.77	2.37	2.63	PKa1: 2-COOH; pKa2: 4-COOH Predicted pKa2: 3.58
Pyrazole-3-carboxylic acid		3.98	3.86	3.74	PKa for COOH
1,2,3-triazole-4-carboxylic acid		3.25	3.35	3.22	PKa for COOH

CLAIMS

We claim:

1. A software implemented methodology for determining the pK_a of a molecule of interest comprising the following steps:

- 5 a. determine the hierarchical atom connectivity tree for each ionizable group on each molecule of a series of molecules for which an experimentally determined pK_a is known;
- b. using the partial least squares statistical methodology, extract coefficients associated with each atom type at each hierarchical level;
- 10 c. determine the hierarchical atom connectivity tree for the molecule of interest; and
- d. multiply the number of occurrences of each atom type in the molecule of interest by the PLS coefficient determined for that atom type and sum the resulting multiplications to obtain the predicted pK_a .

15 2. The method of claim 1 in which each atom type from the hierarchical atom connectivity tree in steps a and c for each ionizable group on each molecule is placed into a separate bin in a bit string.

 3. The method of claim 2 in which the extracted coefficients are associated with the appropriate bin in the bit string.

ABSTRACT

A computer implemented software method enables the prediction of the pK_a of an arbitrary molecule based upon a knowledge of the molecular structure of that molecule and a statistical analysis of the molecular structures of a group of molecules (training set) for which the pK_a is known. Hierarchical atom connectivity trees are constructed for the training set and the various atoms types identified in each molecule are associated in a bit string for that molecule and also associated with the experimentally determined pK_a for that molecule. PLS analysis of the training set data yields coefficients associated with each atom type represented in the bit strings. A hierarchical atom connectivity tree may then be constructed for the molecule of interest. The predicted pK_a is determined by multiplying the number of occurrences of each atom type in the molecule of interest by the PLS coefficient determined for that atom type and summing the resulting multiplications.

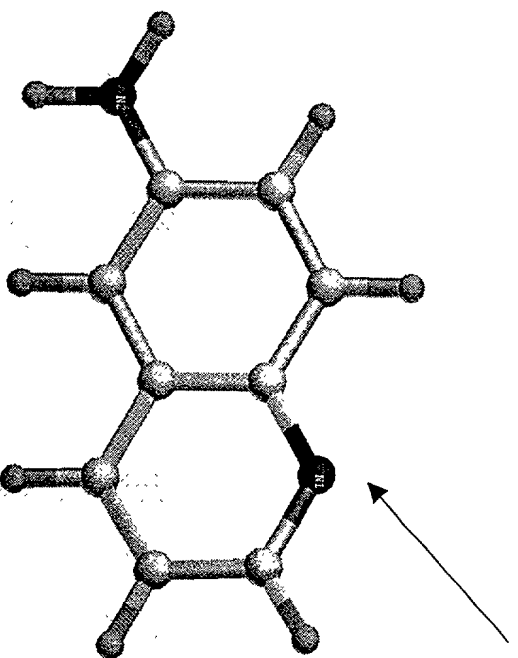
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F16.1

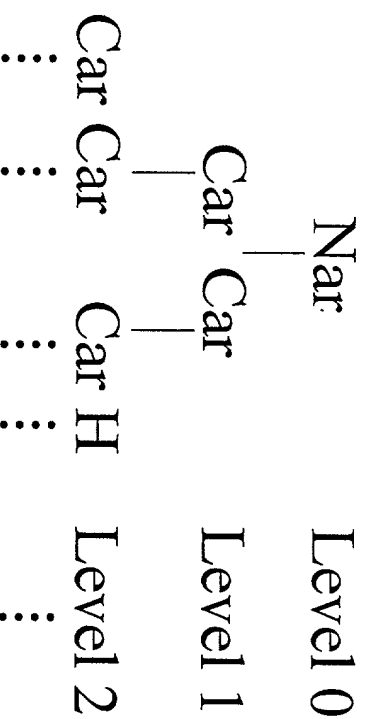
Ionizable Center

- E.g. 6-aminoquinoline

Measured 5.6
predicted 5.0



Start with interesting atom
find connections
find connections to connections
create a tree down to 5 levels
'bin' the atom types for each level
create a 'fingerprint' for this atom



String contains a bin for each required atom type at each level,
the number of atom types is accumulated to form the string

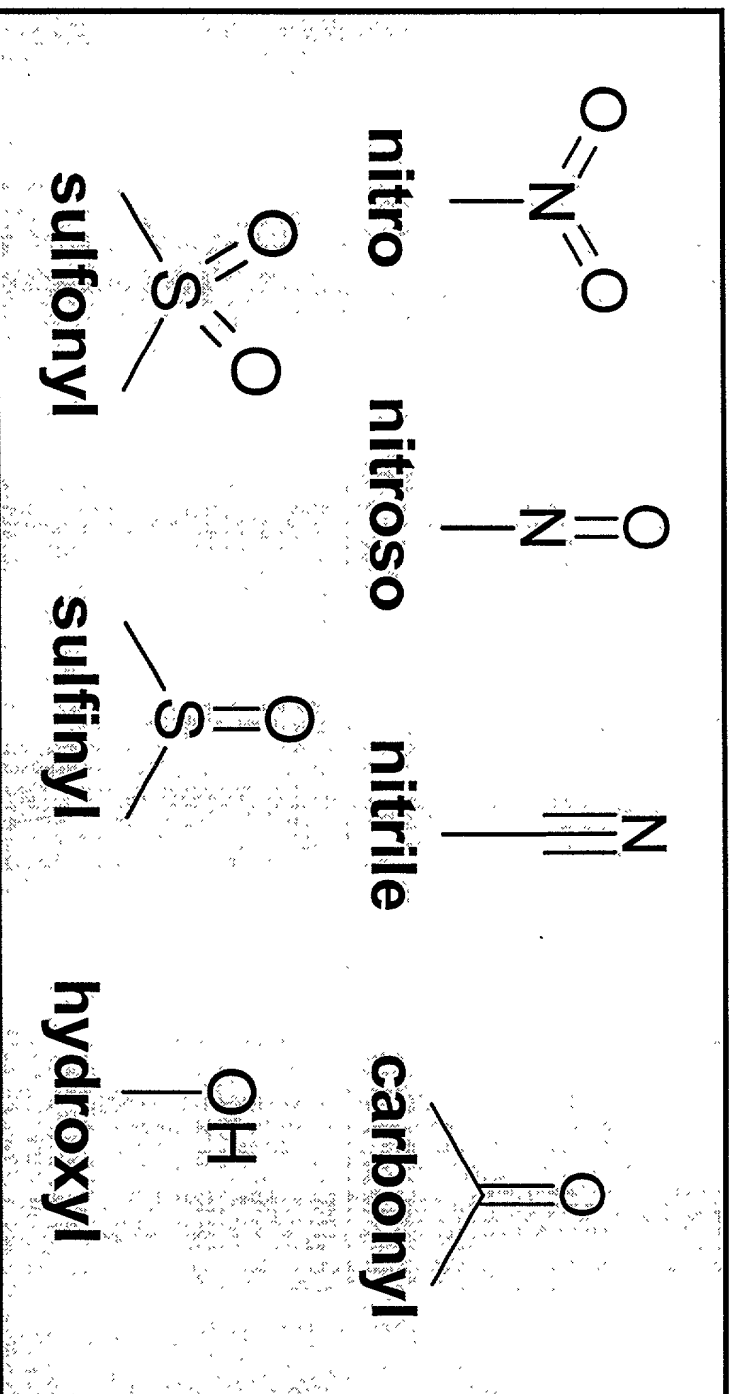
FIG. 2

ATOM TYPES

C.3	sp ³ carbon	H	hydrogen
C.2	sp ² carbon	F	fluorine
C.1	sp ¹ carbon	CL	chlorine
C.ar	aromatic carbon	BR	bromine
C.cat	cationic carbon	I	iodine
N.3	sp ³ nitrogen		
N.2	sp ² nitrogen	<u>Group Types</u>	
N.1	sp ¹ nitrogen	NO ₂	
N.ar	aromatic nitrogen	NO	
N.am	amide nitrogen	CN	
N.pl3	planar sp ³ nitrogen	CO	
N.4	protonated sp ³ nitrogen	SO ₂	
O.3	sp ³ oxygen	SO	
O.2	sp ² oxygen	OH	
O.CO2	oxygen in carboxylate and phosphate groups		
S.3	sp ³ sulfur		
S.2	sp ² sulfur		
S.O	sulfoxide sulfur		
S.O2	sulfone sulfur		
P.3	sp ³ phosphorous		

Environment Around an Ionizable Center

- In addition to atom types, certain group types are also used and improve the performance of the algorithm



F16.3

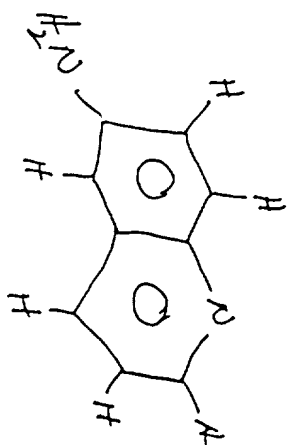
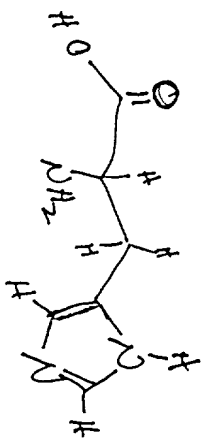


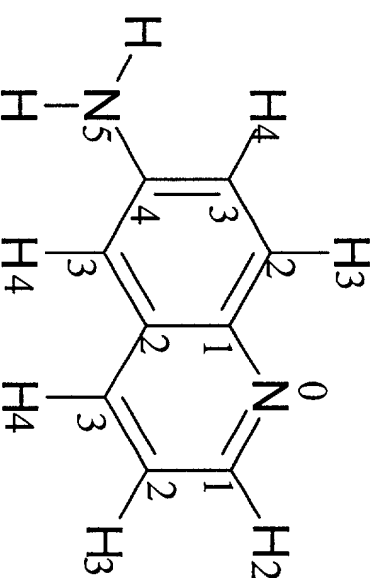
FIG. 4

Atom Type:	C.3	C.2	C.1	C.ar	C.cat	N.3	N.2	N.1	N.ar	N.am	N.pl3	N.4	O.3	O.2	O.CO2	S.3	S.2	S.O	S.O2	P.3	H	F	CL	BR	I	NO2	NO	CN	CO	SO2	SO	OH
Level 0									1																							
Level 1				2																												
Level 2				3																												
Level 3				3																												
Level 4				1																												
Level 5											1																					

FIG. 5



Atom Type:	C.3	C.2	C.1	C.ar	C.cat	N.3	N.2	N.1	N.ar	N.am	N.pl3	N.4	O.3	O.2	O.CO2	S.3	S.2	S.O	S.O2	P.3	H	F	CL	BR	I	NO2	NO	CN	CO	SO2	SO	OH
Level 0							1																									
Level 1		2																			2											
Level 2		1									1																					
Level 3	1																				1											
Level 4	1																				2											
Level 5						1															1								1			



No. of atoms of certain type at each level

	N.ar	C.ar	H	N.pl3
<i>Level 0</i>	1			
<i>Level 1</i>		2		
<i>Level 2</i>		3	1	
<i>Level 3</i>		3	2	
<i>Level 4</i>		1	3	
<i>Level 5</i>				1

Construction of the hierarchical tree from one example, 6-amino quinoline

pK_a of Bases (384)

PC = 5, $r^2=0.922$ $q^2=0.832$, Std. Err = 0.89

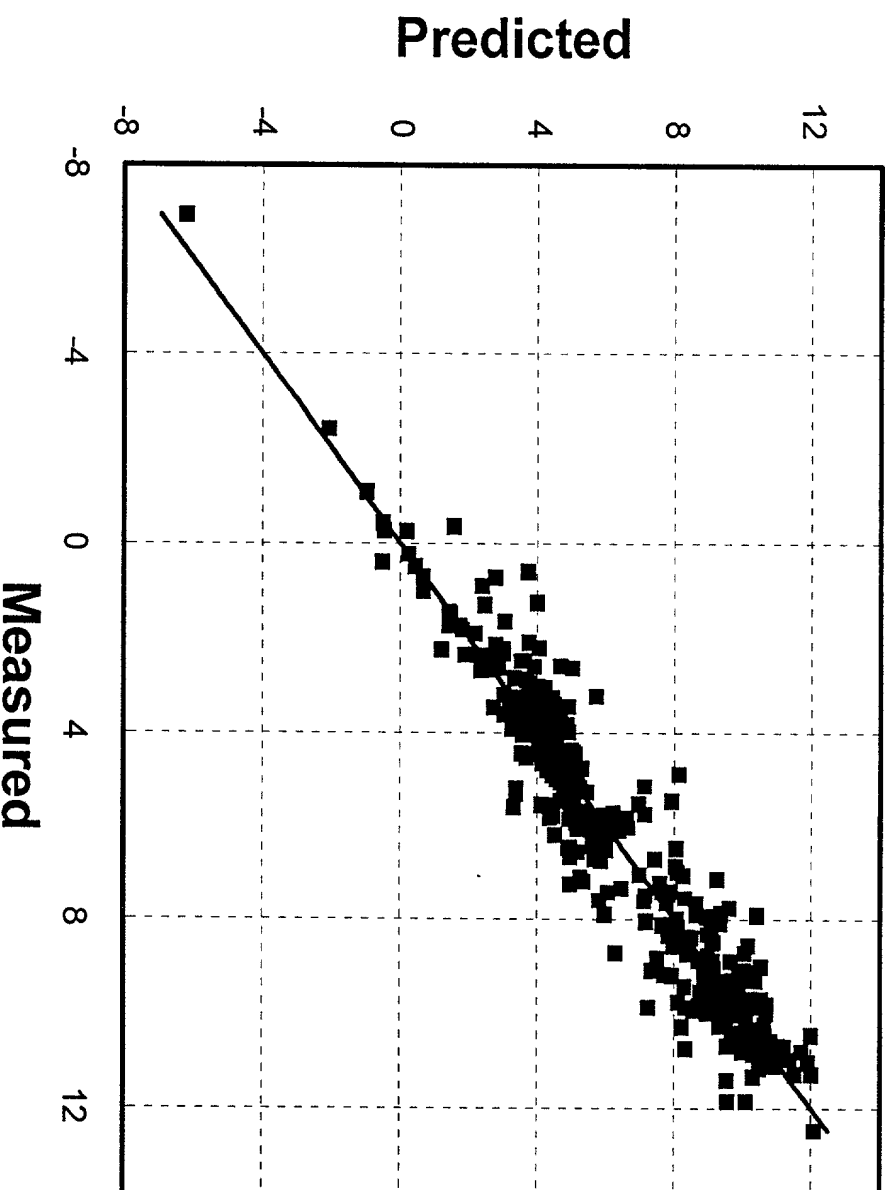


Fig. 7

pK_a of Acids (646)

PC = 6, $r^2 = 0.927$, $q^2 = 0.792$, Std. Err = 0.77

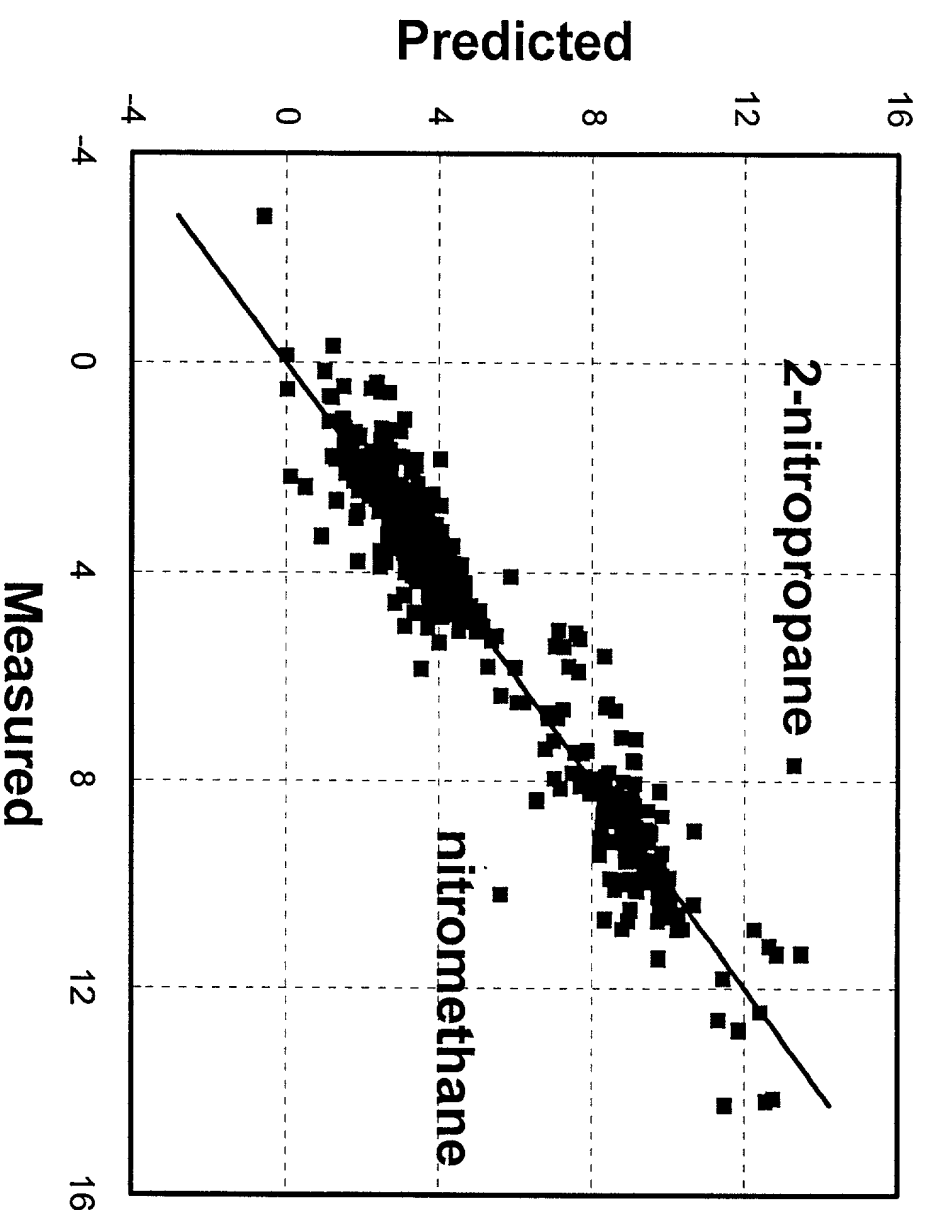
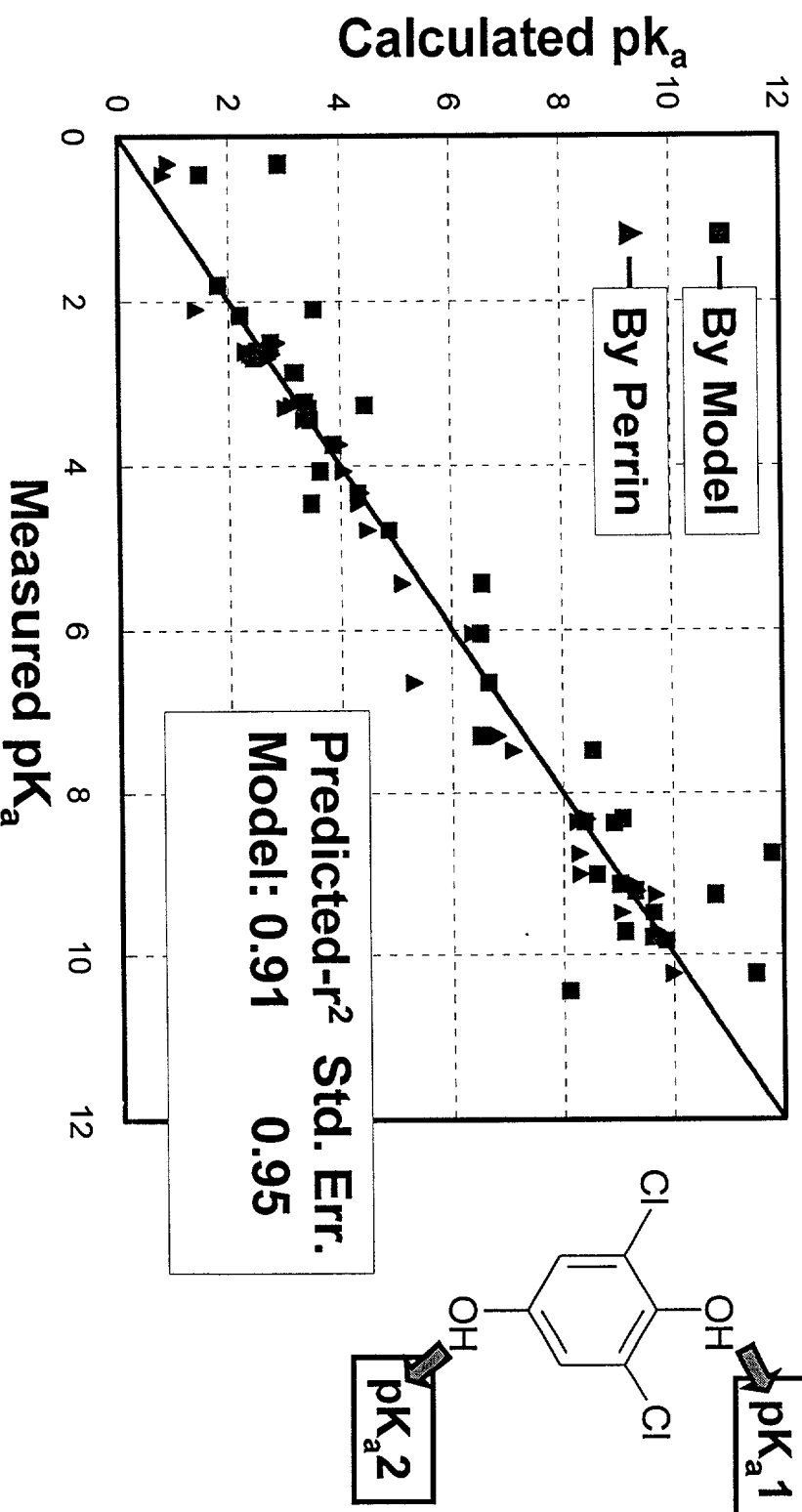


Fig. 8

Prediction on Molecules

- 37 acid and base molecules selected by Perrin* *et al.* as examples, and were not included in the training set
- For molecules containing multiple ionizable centers the model correctly predicted the order for all of them, ie



*Perrin DD, Dempsey B, Serjeant EP, *pKa prediction for organic acids and bases*, Chapman and Hall, London, 1981.